CLEAN VERSION WITH CURRENTLY PENDING CLAIMS

86.   A method of obtaining a plurality of single nucleotide polymorphisms comprising the steps of:

(a)   obtaining a human nucleic acid library comprising a plurality of genomic DNA fragments containing the full human genome or a portion of the human genome comprising at least 100kb of contiguous genomic DNA;

(b)   determining the order of said plurality of genomic DNA fragments in the genome;

(c)   sequencing selected regions of said plurality of genomic DNA fragments; and

(d)   identifying nucleotides in said selected regions which vary between individuals, thereby defining a set of single nucleotide polymorphisms; wherein said plurality of single nucleotide polymorphisms comprises single nucleotide polymorphisms having a heterozygosity rate of at least about 0.18 and having a mean inter-marker spacing of less than 50kb.

87.   A method of obtaining a plurality of single nucleotide polymorphisms comprising the steps of:

(a)   obtaining a human nucleic acid library comprising a plurality of genomic DNA fragments containing the full human genome or a portion of the human genome comprising at least 100kb of contiguous genomic DNA;

(b)   determining the order of said plurality of genomic DNA fragments in the genome;

(c)   sequencing selected regions of said plurality of genomic DNA fragments; and

(d)   identifying nucleotides in said selected regions which vary between individuals, thereby defining a set of single nucleotide polymorphisms; wherein said plurality of single nucleotide polymorphisms comprises single nucleotide polymorphisms having a heterozygosity rate of at least about 0.18 and having a mean inter-marker spacing of less than 50kb.

89.   The method of Claim 86, further comprising identifying two or more single nucleotide polymorphisms per genomic DNA fragment. .

92.   The method of Claim 86, further comprising selecting single nucleotide polymorphisms having a heterozygosity rate of about 0.32.

93. The method of Claim 86, further comprising selecting single nucleotide polymorphisms having a heterozygosity rate of about 0.42.

94. The method of Claim 86, wherein said identifying step comprises identifying at least 20,000 signle nucleotide polymorphisms.

95. The method of Claim 86, wherein the step of determining the sequence of selected regions of said plurality of genomic DNA fragments comprises inserting fragments of said plurality of genomic DNA fragments into a vector to generate a plurality of subclones and determining the sequence of a regions of the inserts in said plurality of subclones or a subset thereof.

96. The method of Claim 86, wherein a set of about 10,000 to about 30,000 genomic DNA inserts with an average size between 100kb and 300kb are ordered.

97. The method of Claim 86, further comprising determining the position of said single nucleotide polymorphisms along the genome or a portion of the genome.

98. The method of Claim 86, further comprising obtaining pluralities of single nucleotide polymorphisms such that each single nucleotide polymorphism is in linkage disequilibrium with at least one of said identified single nucleotide polymorphism.

99. The method of Claim 86, wherein said portion of the genome comprises at least 200 kb of contiguous genomic DNA.

100. The method of Claim 86, wherein wherein said portion of the genome comprises at least 2 MB of contiguous genomic DNA.

101. The method of Claim 86, wherein wherein said portion of the genome comprises at least 20 Mb of contiguous genomic DNA.

102. The method of Claim 86, further comprising the step of identifying one or more groups of single nucleotide polymorphisms which are in linkage disequilibrium with one another.

103. The method of Claim 86, further comprising the step of identifying one or more groups of single nucleotide polymorphisms wherein the single nucleotide polymorphisms in each of these groups are located within a genomic region spanning from 1 to 5kb.

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104. The method of Claim 86, further comprising the step of identifying one or more groups of single nucleotide polymorphisms wherein the single nucleotide polymorphisms in each of these groups are located within a genomic region spanning from50 to 150kb.

105. The method of Claim 86, further comprising the step of identifying one or more groups of single nucleotide polymorphisms wherein the single nucleotide polymorphisms in each of these groups are located within a genomic region spanning more than 1Mb.

122. (New) A map produced by the method of Claim 86.